CLAIMS

1. A nucleic acid encoding a modified xylanase comprising a polypeptide having an amino acid sequence as set forth in SEQ ID NO:1, wherein the sequence has at least one substituted amino acid residue at a position selected from the group consisting of: 2, 5, 7, 10 , 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191.

2. The nucleic acid according to Claim 1, wherein the substitution is selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

3. The nucleic acid according to Claim 2, wherein the xylanase has at least one substitution selected from the group consisting of: H22K, S65C, N92C, F93W, N97R, V108H, H144C, H144K, F180Q and S186C.

4. The nuclec acid according to Claim 3, wherein the xylanase has the following mutations: F93W, N97R and H144K.

5. The nucleic acid according to Claim 3, wherein the xylanase has the following mutations: H144C and N92K.

6. The nucleic acid according to Claim 3, wherein the xylanase has the following mutations: F180Q, H144C and N92C.

7. The nucleic acid according to Claim 3, wherein the xylanase has the following mutations: H22K and F180Q.

8. The nucleic acid according to Claim 3, wherein the xylanase has the following mutations: V108H.

9. The nuceic acid according to Claim 3, wherein the xylanase has the following mutations: S65C and S186C.

10. The nucleic acid according to Claim 3, wherein the xylanase has the following mutations: H22K, F180Q, H144C and N92C.

11. A modified xylanase comprising a polypeptide having an amino acid sequence as set forth in SEQ ID NO:1, wherein the sequence has at least one substituted amino acid residue at a position selected from the group consisting of: 2, 5, 7, 10 , 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191.

12. The xylanase according to Claim 11, wherein the substitution is selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

13. The xylanase according to Claim 12, wherein the modified xylanase has at least one substitution selected from the group consisting of: H22K, S65C, N92C, F93W, N97R, V108H, H144C, H144K, F180Q and S186C.

14. The xylanase according to Claim 13, wherein the xylanase has the following mutations: F93W, N97R and H144K.

15. The xylanase according to Claim 13, wherein the xylanase has the following mutations: H144C and N92K.

16. The xylanase according to Claim 13, wherein the xylanase has the following mutations: F180Q, H144C and N92C.

17. The xylanase according to Claim 13, wherein the xylanase has the following mutations: H22K and F180Q.

18. The xylanase according to Claim 13, wherein the xylanase has the following mutations: V108H.

19. The xylanase according to Claim 13, wherein the xylanase has the following mutations: S65C and S186C.

20. The xylanase according to Claim 13, wherein the xylanase has the following mutations: H22K, F180Q, H144C and N92C.

21. A modified enzyme, the modified enzyme comprising an amino acid sequence, the amino acid sequence being homologous to the sequence set forth in SEQ ID NO:1, the amino acid sequence having at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 5, 7, 10 , 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38, 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191.

22. The enzyme according to Claim 21, wherein homology to the sequence set forth in SEQ ID NO:1 is at least 20%.

23. The enzyme according to Claim 22, wherein the amino acid sequence has at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

24. A glycosyl hydrolase of Clan C comprising an amino acid sequence, the amino acid sequence being homologous to the sequence set forth in SEQ ID NO:1, the amino acid sequence having at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 5, 7, 10 , 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38 , 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191.

25. The glycosyl hydrolase according to Claim 24, wherein homology to the sequence set forth in SEQ ID NO:1 is at least 20%.

26. The glycosyl hydrolase according to Claim 25, wherein the amino acid sequence has at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

27. A modified family 11 xylanase comprising an amino acid sequence, the amino acid sequence being homologous to the sequence set forth in SEQ ID NO:1, the amino acid sequence having at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 5, 7, 10 , 11, 16, 19, 22,

26, 28, 29, 30, 34, 36, 38 , 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191.

28. The xylanase according to Claim 27, wherein homology to the sequence set forth in SEQ ID NO:1 is at least 20%.

29. The xylanase according to Claim 28, wherein the amino acid sequence has at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.

30. A family 12 cellulase comprising an amino acid sequence, the amino acid sequence being homologous to the sequence set forth in SEQ ID NO:1, the amino acid sequence having at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 5, 7, 10 , 11, 16, 19, 22, 26, 28, 29, 30, 34, 36, 38 , 57, 58, 61, 63, 65, 67, 92, 93, 97, 105, 108, 110, 111, 113, 132, 143, 144, 147, 149, 151, 153, 157, 160, 162, 165, 169, 180, 184, 186, 188, 190 and +191.

31. The cellulose according to Claim 30, wherein homology to the sequence set forth in SEQ ID NO:1 is at least 20%.

32. The cellulose according to Claim 31, wherein the amino acid sequence has at least one substituted amino acid residue at a position equivalent to a position selected from the group consisting of: 2, 22, 28, 58, 65, 92, 93, 97, 105, 108, 144, 162, 180, 186 and +191.